

Influenza A viruses circulating in pigs and pig farmers of Switzerland

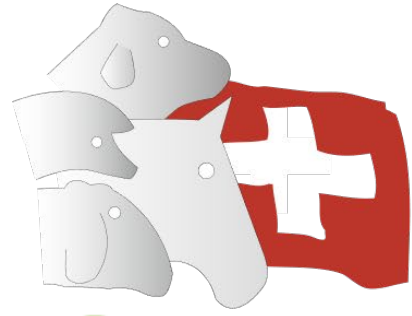
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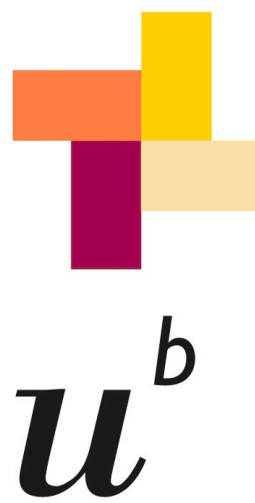
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Objectives

- Influenza A Viruses (IAVs) in pigs are candidates for future human pandemics because of high prevalence in pig herds and contact persons
- Knowledge about IAVs in pigs in Switzerland is limited

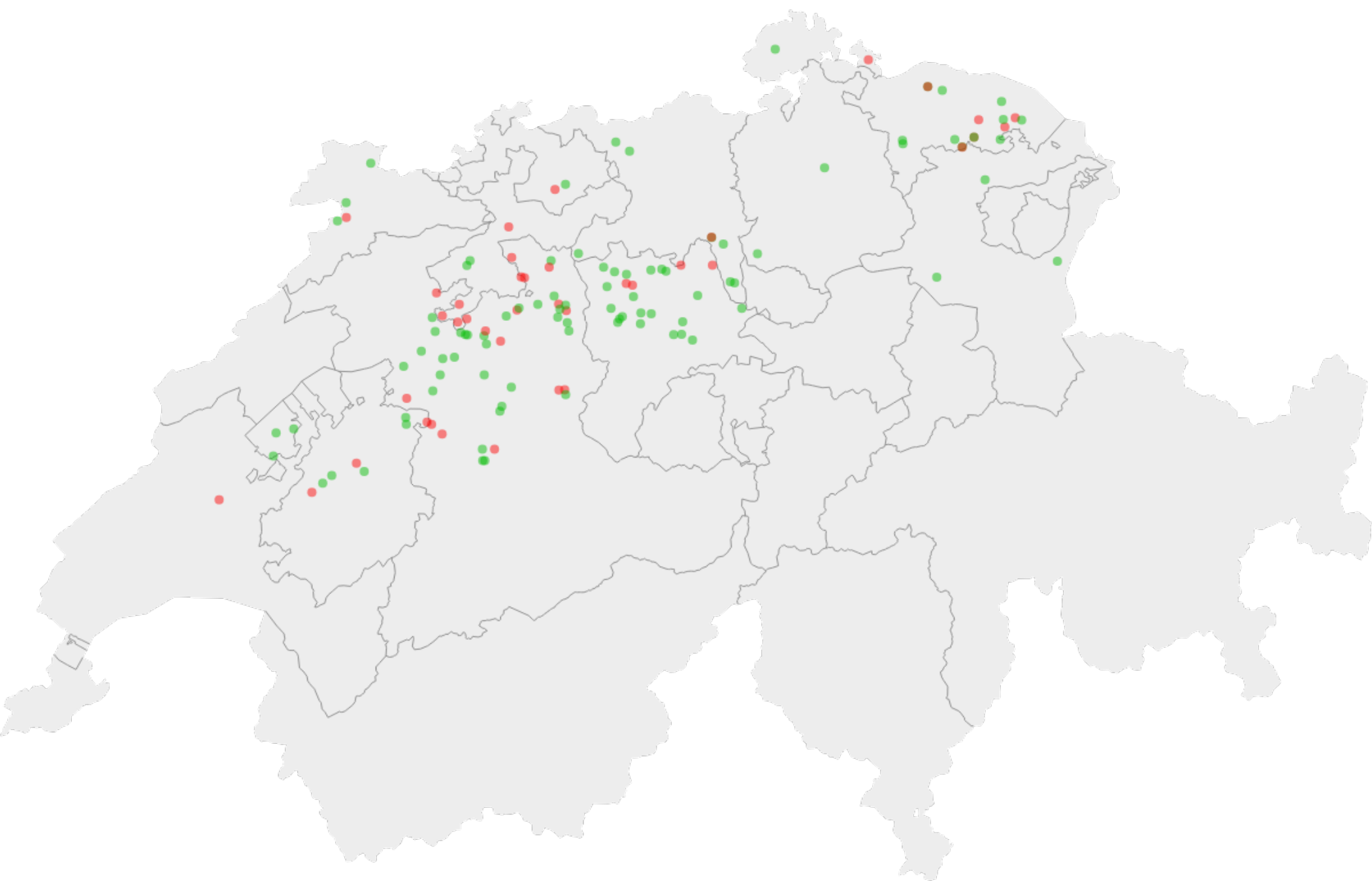
Aims: creating a phylogenetic and epidemiologic profile by examining pig herds with and without respiratory clinical signs & diseased pig caretakers

- pan-IAV qPCR screening of IAVs and whole genome sequencing
- epidemiologic questionnaire (data not presented)

Material & Methods

Study type and population

- Swiss pig population with all production types
- Cohort study of 100 pig herds sampled actively (14 with respiratory signs, 86 without)
- Respiratory diseased pig herds sampled passively after reports of veterinarians (25 with respiratory signs)



Herds with clinical signs
Herds without clinical signs

Figure 1: Pig herds included in study, distributed across all areas with high pig density in Switzerland

260 epidemiologic parameters collected through a questionnaire and clinical herd examination (data not presented)

Sampling scheme: Nasal swabs

- 19 weaners (4-12 weeks of age) in herds of cohort study
- 5 pigs with respiratory signs in herds with reported symptoms

Laboratory Analyses:

- panIAV RT-qPCR of matrix gene segment (cut-off for positives set at Cp 38 ^{1,2})
- RT-PCR to amplify all 8 segments of positive samples³
- Whole genome sequencing and phylogenetic analysis⁴

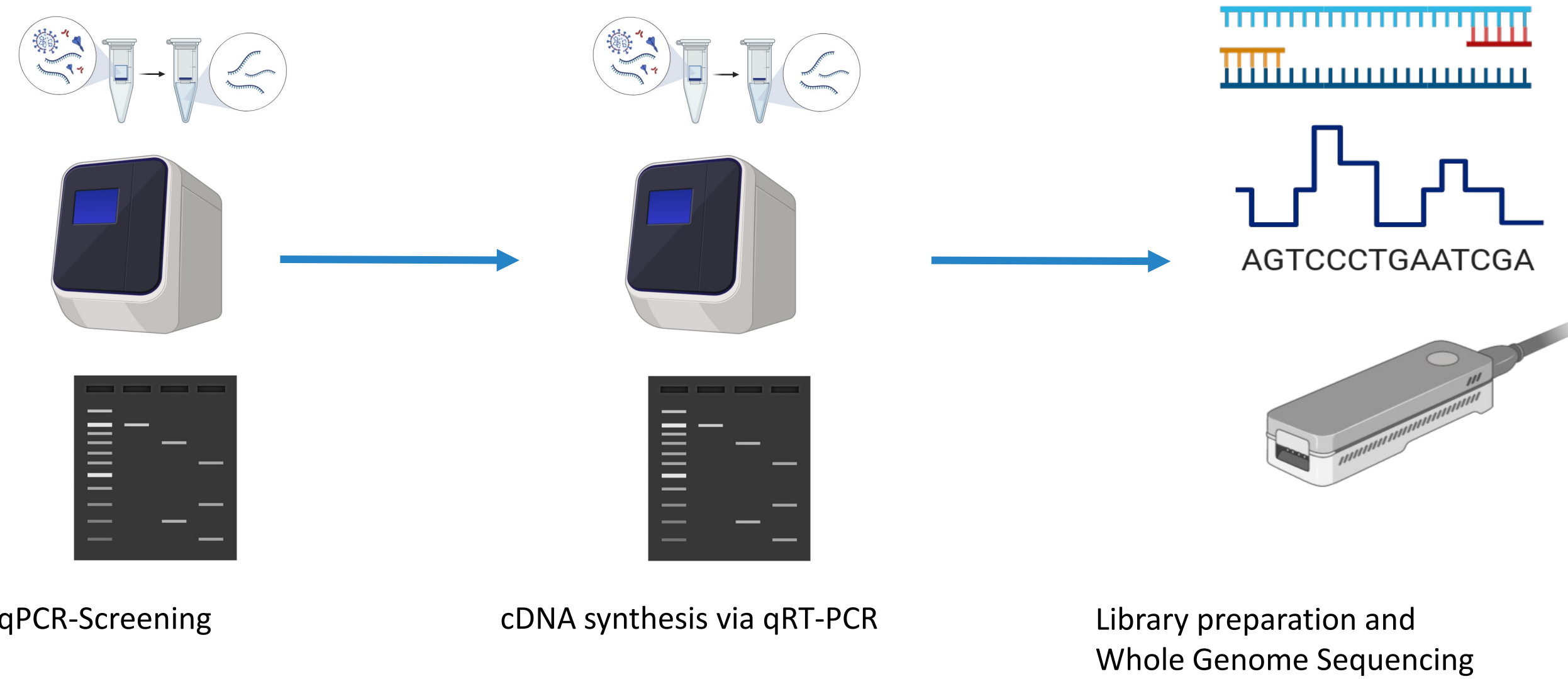


Figure 2: Workflow of laboratory analyses

Conclusions

- Swine IAVs are widely prevalent in Swiss pig herds and seem to occur without causing clinical signs at all times.
- Swiss pig herds are infected with a single variant of swIAV H1N1 EA lineage. IAVs show little diversity and appear distinct from neighboring countries.
- A potential zoonotic transmission between pigs and a farmer underlines the risk of pig-human transmission.

Results

101 herds screened by qPCR and 40 full genomes sequenced

- 34 (33.7%) herds tested positive for IAV, 140 of 1576 samples (8,9%)
 - 15/30 (50.0%) herds with clinical signs
 - 19/71 (26.8%) herds without clinical signs

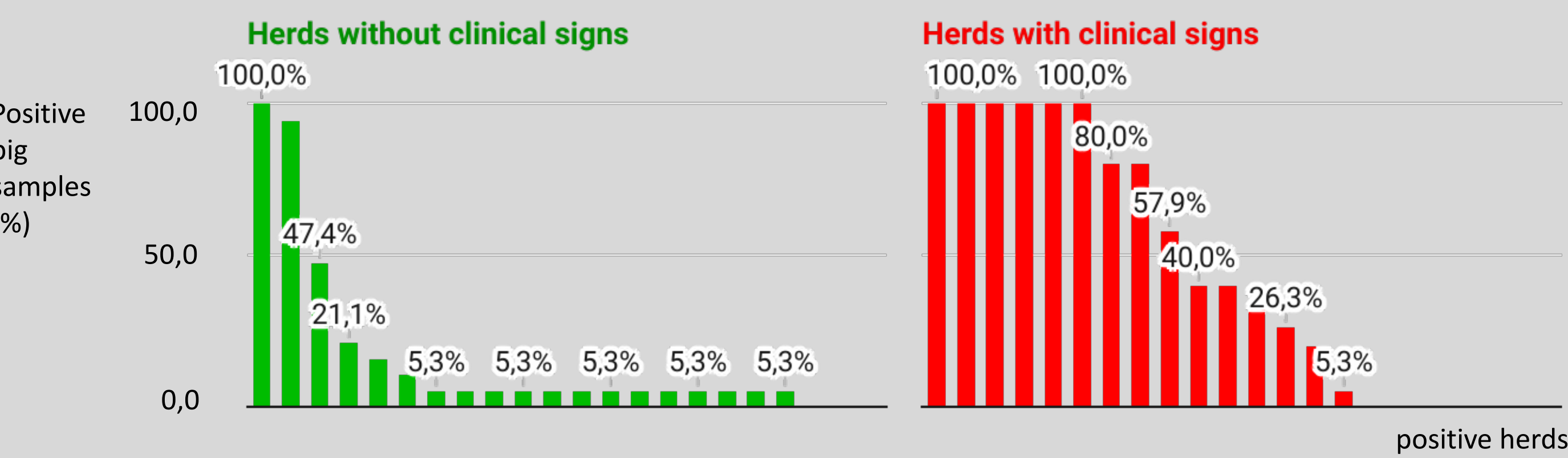
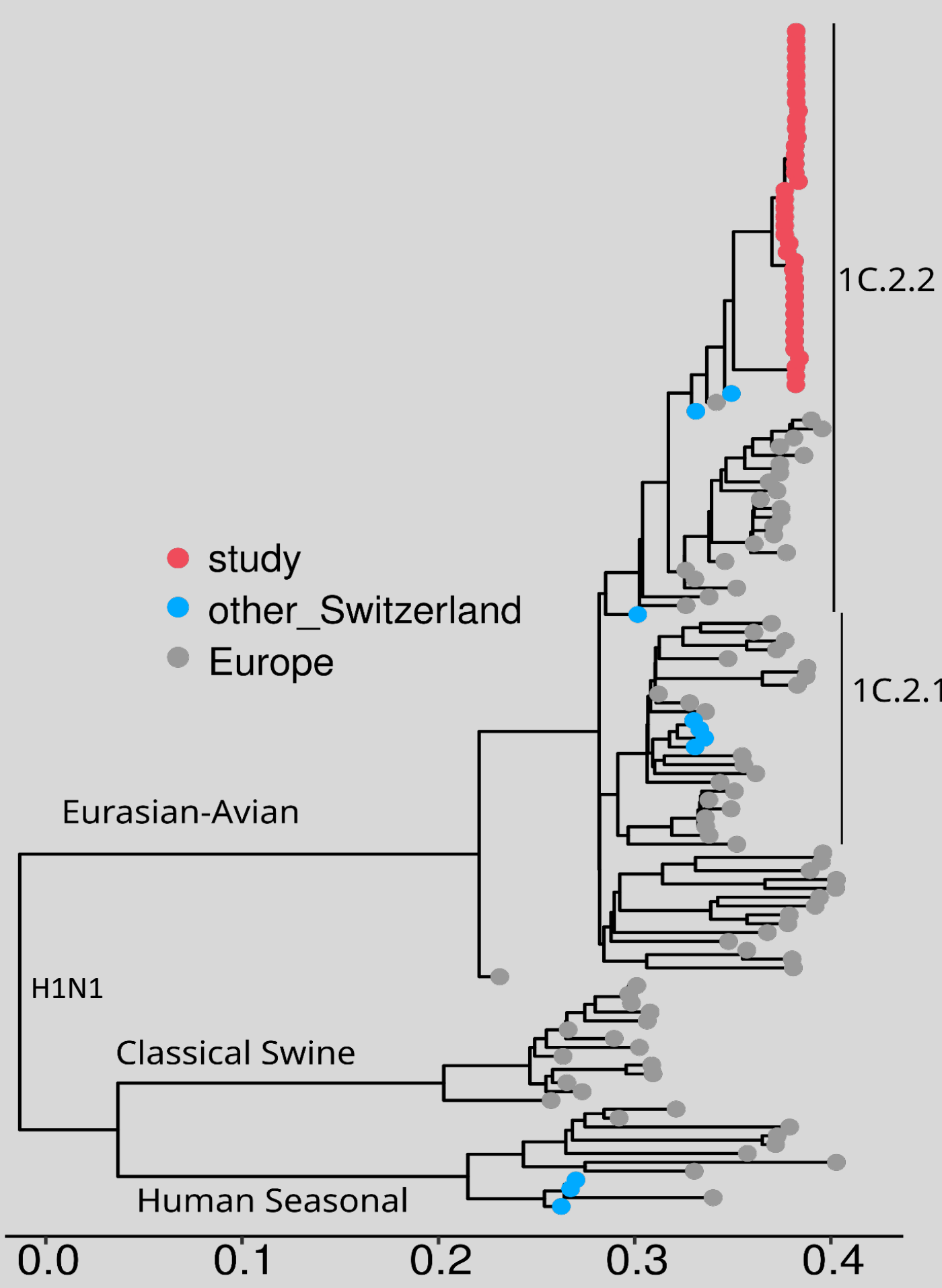


Figure 3: Percentage of positive pig samples per herd, diseased herds with bigger percentage of pigs testing positive per herd

- Detection of Swine IAVs, subtype (H1N1), Eurasian avian lineage, clade 1 C.2.2
 - Monophyletic cluster, diversity to previous Swiss sequences

→ No introduction of IAVs via imports of live pigs detected
→ No human-pig transmission of H1H1_09_pdm lineage observed

Figure 4: Maximum-Likelihood phylogenetic tree of the HA gene segment of successfully sequenced positive samples



- Zoonotic transmission event between pig herd and farmer

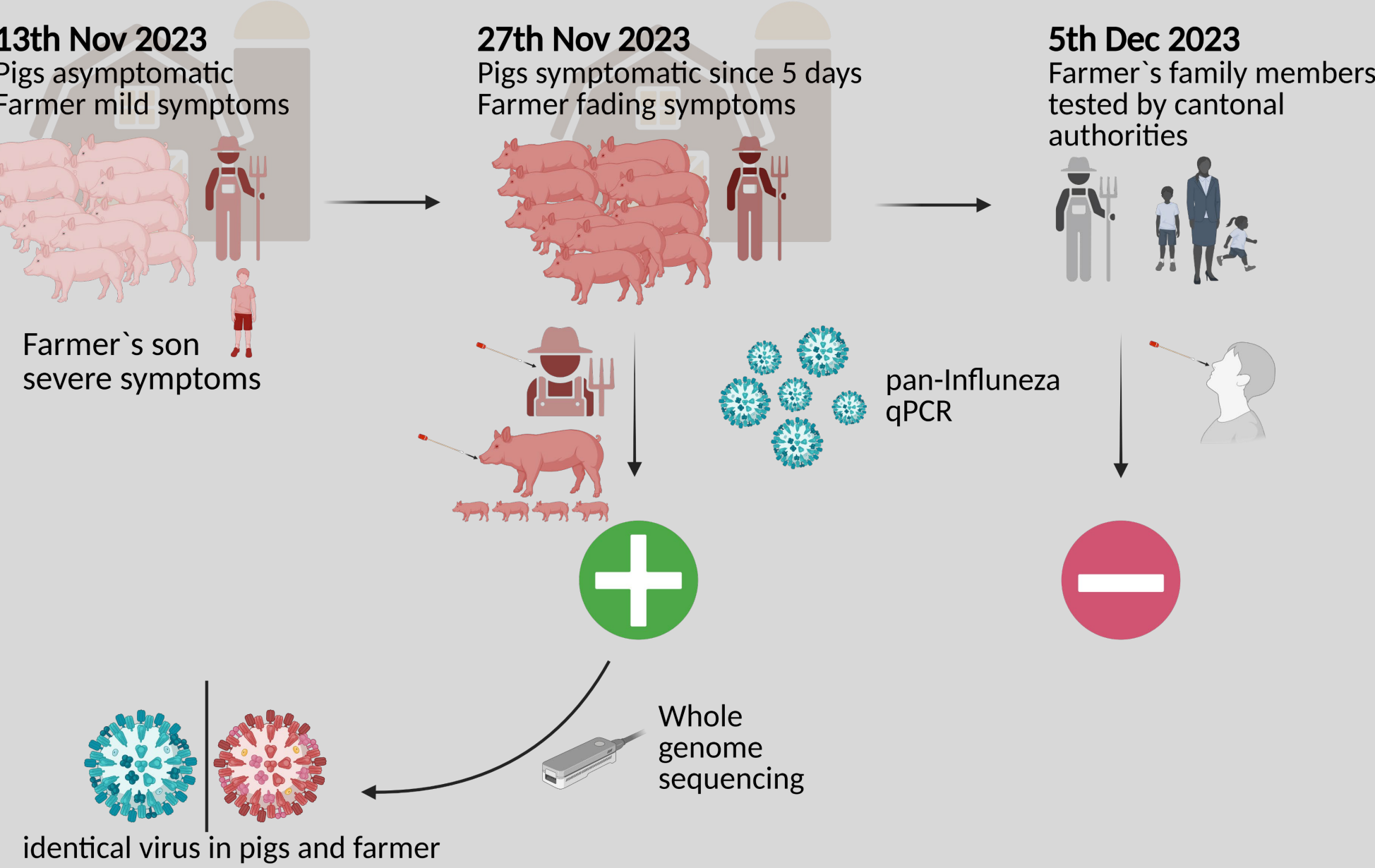


Figure 5: Timeline of zoonotic event

References

1 Nagy A, Černíková L, Kunteová K, et al. A universal RT-qPCR assay for "One Health" detection of influenza A viruses. PLoS One. 2021;16(1):e0244669.
2 Paula Lagan, Michael Hamill, Susan Cull, Anthony Hanrahan, Rosanna M Wregor, Ken Lemon, Swine influenza A virus infection dynamics and evolution in intensive pig production systems, Virus Evolution, Volume 10, Issue 1, 2024, vead017.
3 Zhou, B., Donnelly, M. E., Scholes, D. T., St. George, K., Hatta, M., Kawakita, Y., & Wentworth, D. E. (2009). Single-Reaction Genomic Amplification Accelerates Sequencing and Vaccine Production for Classical and Swine Origin Human Influenza A Viruses. Journal of Virology, 83(19), 10309–10313.
4 Licheri M, Licheri MF, Mwanga M, et al. Optimized workflow for high-throughput whole genome surveillance of influenza A virus. Published online October 25, 2024.
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